

SEQUENCE LISTING

<110> IMMUNEX CORPORATION
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Zhou, Hongxing

<120> ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR

<130> 3492-WO

<140> --to be assigned--

<141> 2004-11-04

<150> 60/518,166

<151> 2003-11-07

<160> 77

<170> PatentIn version 3.2

<210> 1

<211> 2475

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (1)..(2475)

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Leu Leu Gln Val Ala Ser Ser Gly Asn Met Lys Val Leu Gln Glu Pro
20 25 30
acc tgc gtc tcc gac tac atg agc atc tct act tgc gag tgg aag atg 144
Thr Cys Val Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met
35 40 45
aat ggt ccc acc aat tgc agc acc gag ctc cgc ctg ttg tac cag ctg 192
Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu
50 55 60
gtt ttt ctg ctc tcc gaa gcc cac acg tgt atc cct gag aac aac gga 240
Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly
65 70 75 80
ggc gcg ggg tgc gtg tgc cac ctg ctc atg gat gac gtg gtc agt gcg 288
Gly Ala Gly Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala
85 90 95
gat aac tat aca ctg gac ctg tgg gct ggg cag cag ctg ctg tgg aag 336
Asp Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys
100 105 110

ggc tcc ttc aag ccc agc gag cat gtg aaa ccc agg gcc cca gga aac Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn 115 120 125	384
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aac ccg tat ccc cct gac aat tac ctg tat aat cat ctc acc tat gca Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala 145 150 155 160	480
gtc aac att tgg agt gaa aac gac ccg gca gat ttc aga atc tat aac Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn 165 170 175	528
gtg acc tac cta gaa ccc tcc ctc cgc atc gca gcc agc acc ctg aag Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys 180 185 190	576
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tac agg gag ccc ttc gag cag cac ctc ctg ctg ggc gtc agc gtt tcc Tyr Arg Glu Pro Phe Glu Gln His Leu Leu Leu Gly Val Ser Val Ser 225 230 235 240	720
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cca gag agc atc agc gtg gtg cga tgt gtg gag ttg ttt gag gcc ccg	1104
Pro Glu Ser Ile Ser Val Val Arg Cys Val Glu Leu Phe Glu Ala Pro	
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Val Glu Cys Glu Glu Glu Glu Glu Val Glu Glu Glu Lys Gly Ser Phe	
370 375 380	
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Cys Ala Ser Pro Glu Ser Ser Arg Asp Asp Phe Gln Glu Gly Arg Glu	
385 390 395 400	
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Gly Ile Val Ala Arg Leu Thr Glu Ser Leu Phe Leu Asp Leu Leu Gly	
405 410 415	
gag gag aat ggg ggc ttt tgc cag cag gac atg ggg gag tca tgc ctt	1296
Glu Glu Asn Gly Gly Phe Cys Gln Gln Asp Met Gly Glu Ser Cys Leu	
420 425 430	
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Leu Pro Pro Ser Gly Ser Thr Ser Ala His Met Pro Trp Asp Glu Phe	
435 440 445	
cca agt gca ggg ccc aag gag gca cct ccc tgg ggc aag gag cag cct	1392
Pro Ser Ala Gly Pro Lys Glu Ala Pro Pro Trp Gly Lys Glu Gln Pro	
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ctc cac ctg gag cca agt cct cct gcc agc ccg acc cag agt cca gac	1440
Leu His Leu Glu Pro Ser Pro Pro Ala Ser Pro Thr Gln Ser Pro Asp	
465 470 475 480	
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Asn Leu Thr Cys Thr Glu Thr Pro Leu Val Ile Ala Gly Asn Pro Ala	
485 490 495	
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Tyr Arg Ser Phe Ser Asn Ser Leu Ser Gln Ser Pro Cys Pro Arg Glu	
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Leu Gly Pro Asp Pro Leu Leu Ala Arg His Leu Glu Glu Val Glu Pro	
515 520 525	
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Glu Met Pro Cys Val Pro Gln Leu Ser Glu Pro Thr Thr Val Pro Gln	
530 535 540	
cct gag cca gaa acc tgg gag cag atc ctc cgc cga aat gtc ctc cag	1680
Pro Glu Pro Glu Thr Trp Glu Gln Ile Leu Arg Arg Asn Val Leu Gln	
545 550 555 560	
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His Gly Ala Ala Ala Ala Pro Val Ser Ala Pro Thr Ser Gly Tyr Gln	
565 570 575	
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Glu Phe Val His Ala Val Glu Gln Gly Gly Thr Gln Ala Ser Ala Val	
580 585 590	

gtg ggc ttg ggt ccc cca gga gag gct ggt tac aag gcc ttc tca agc	1824
Val Gly Leu Gly Pro Pro Gly Glu Ala Gly Tyr Lys Ala Phe Ser Ser	
595 600 605	
ctg ctt gcc agc agt gct gtg tcc cca gag aaa tgt ggg ttt ggg gct	1872
Leu Leu Ala Ser Ser Ala Val Ser Pro Glu Lys Cys Gly Phe Gly Ala	
610 615 620	
agc agt ggg gaa gag ggg tat aag cct ttc caa gac ctc att cct ggc	1920
Ser Ser Gly Glu Glu Gly Tyr Lys Pro Phe Gln Asp Leu Ile Pro Gly	
625 630 635 640	
tgc cct ggg gac cct gcc cca gtc cct gtc ccc ttg ttc acc ttt gga	1968
Cys Pro Gly Asp Pro Ala Pro Val Pro Val Pro Leu Phe Thr Phe Gly	
645 650 655	
ctg gac agg gag cca cct cgc agt ccg cag agc tca cat ctc cca agc	2016
Leu Asp Arg Glu Pro Pro Arg Ser Pro Gln Ser Ser His Leu Pro Ser	
660 665 670	
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675 680 685	
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Met Pro Lys Pro Pro Leu Pro Gln Glu Gln Ala Thr Asp Pro Leu Val	
690 695 700	
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Asp Ser Leu Gly Ser Gly Ile Val Tyr Ser Ala Leu Thr Cys His Leu	
705 710 715 720	
tgc ggc cac ctg aaa cag tgt cat ggc cag gag gat ggt ggc cag acc	2208
Cys Gly His Leu Lys Gln Cys His Gly Gln Glu Asp Gly Gly Gln Thr	
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cct gtc atg gcc agt cct tgc tgt ggc tgc tgc tgt gga gac agg tcc	2256
Pro Val Met Ala Ser Pro Cys Cys Gly Cys Cys Cys Gly Asp Arg Ser	
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Ser Pro Pro Thr Thr Pro Leu Arg Ala Pro Asp Pro Ser Pro Gly Gly	
755 760 765	
gtt cca ctg gag gcc agt ctg tgt ccg gcc tcc ctg gca ccc tcg ggc	2352
Val Pro Leu Glu Ala Ser Leu Cys Pro Ala Ser Leu Ala Pro Ser Gly	
770 775 780	
atc tca gag aag agt aaa tcc tca tca tcc ttc cat cct gcc cct ggc	2400
Ile Ser Glu Lys Ser Lys Ser Ser Ser Ser Phe His Pro Ala Pro Gly	
785 790 795 800	
aat gct cag agc tca agc cag acc ccc aaa atc gtg aac ttt gtc tcc	2448
Asn Ala Gln Ser Ser Ser Gln Thr Pro Lys Ile Val Asn Phe Val Ser	
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gtg gga ccc aca tac atg agg gtc tct	2475
Val Gly Pro Thr Tyr Met Arg Val Ser	
820 825	

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 <212> PRT
 <213> Homo sapien

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Thr Cys Val Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met
 35 40 45

Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu
 50 55 60

Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly
 65 70 75 80

Gly Ala Gly Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala
 85 90 95

Asp Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys
 100 105 110

Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn
 115 120 125

Leu Thr Val His Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser
 130 135 140

Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala
 145 150 155 160

Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn
 165 170 175

Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys
 180 185 190

Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr
 195 200 205

Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser
 210 215 220

Tyr Arg Glu Pro Phe Glu Gln His Leu Leu Leu Gly Val Ser Val Ser
225 230 235 240

Cys Ile Val Ile Leu Ala Val Cys Leu Leu Cys Tyr Val Ser Ile Thr
245 250 255

Lys Ile Lys Lys Glu Trp Trp Asp Gln Ile Pro Asn Pro Ala Arg Ser
260 265 270

Arg Leu Val Ala Ile Ile Ile Gln Asp Ala Gln Gly Ser Gln Trp Glu
275 280 285

Lys Arg Ser Arg Gly Gln Glu Pro Ala Lys Cys Pro His Trp Lys Asn
290 295 300

Cys Leu Thr Lys Leu Leu Pro Cys Phe Leu Glu His Asn Met Lys Arg
305 310 315 320

Asp Glu Asp Pro His Lys Ala Ala Lys Glu Met Pro Phe Gln Gly Ser
325 330 335

Gly Lys Ser Ala Trp Cys Pro Val Glu Ile Ser Lys Thr Val Leu Trp
340 345 350

Pro Glu Ser Ile Ser Val Val Arg Cys Val Glu Leu Phe Glu Ala Pro
355 360 365

Val Glu Cys Glu Glu Glu Glu Glu Val Glu Glu Glu Lys Gly Ser Phe
370 375 380

Cys Ala Ser Pro Glu Ser Ser Arg Asp Asp Phe Gln Glu Gly Arg Glu
385 390 395 400

Gly Ile Val Ala Arg Leu Thr Glu Ser Leu Phe Leu Asp Leu Leu Gly
405 410 415

Glu Glu Asn Gly Gly Phe Cys Gln Gln Asp Met Gly Glu Ser Cys Leu
420 425 430

Leu Pro Pro Ser Gly Ser Thr Ser Ala His Met Pro Trp Asp Glu Phe
435 440 445

Pro Ser Ala Gly Pro Lys Glu Ala Pro Pro Trp Gly Lys Glu Gln Pro
450 455 460

Leu His Leu Glu Pro Ser Pro Pro Ala Ser Pro Thr Gln Ser Pro Asp
 465 470 475 480

Asn Leu Thr Cys Thr Glu Thr Pro Leu Val Ile Ala Gly Asn Pro Ala
 485 490 495

Tyr Arg Ser Phe Ser Asn Ser Leu Ser Gln Ser Pro Cys Pro Arg Glu
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Leu Gly Pro Asp Pro Leu Leu Ala Arg His Leu Glu Glu Val Glu Pro
 515 520 525

Glu Met Pro Cys Val Pro Gln Leu Ser Glu Pro Thr Thr Val Pro Gln
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Pro Glu Pro Glu Thr Trp Glu Gln Ile Leu Arg Arg Asn Val Leu Gln
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His Gly Ala Ala Ala Pro Val Ser Ala Pro Thr Ser Gly Tyr Gln
 565 570 575

Glu Phe Val His Ala Val Glu Gln Gly Gly Thr Gln Ala Ser Ala Val
 580 585 590

Val Gly Leu Gly Pro Pro Gly Glu Ala Gly Tyr Lys Ala Phe Ser Ser
 595 600 605

Leu Leu Ala Ser Ser Ala Val Ser Pro Glu Lys Cys Gly Phe Gly Ala
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Ser Ser Gly Glu Glu Gly Tyr Lys Pro Phe Gln Asp Leu Ile Pro Gly
 625 630 635 640

Cys Pro Gly Asp Pro Ala Pro Val Pro Val Pro Leu Phe Thr Phe Gly
 645 650 655

Leu Asp Arg Glu Pro Pro Arg Ser Pro Gln Ser Ser His Leu Pro Ser
 660 665 670

Ser Ser Pro Glu His Leu Gly Leu Glu Pro Gly Glu Lys Val Glu Asp
 675 680 685

Met Pro Lys Pro Pro Leu Pro Gln Glu Gln Ala Thr Asp Pro Leu Val
 690 695 700

Asp Ser Leu Gly Ser Gly Ile Val Tyr Ser Ala Leu Thr Cys His Leu
705 710 715 720

Cys Gly His Leu Lys Gln Cys His Gly Gln Glu Asp Gly Gly Gln Thr
725 730 735

Pro Val Met Ala Ser Pro Cys Cys Gly Cys Cys Cys Gly Asp Arg Ser
740 745 750

Ser Pro Pro Thr Thr Pro Leu Arg Ala Pro Asp Pro Ser Pro Gly Gly
755 760 765

Val Pro Leu Glu Ala Ser Leu Cys Pro Ala Ser Leu Ala Pro Ser Gly
770 775 780

Ile Ser Glu Lys Ser Lys Ser Ser Ser Ser Phe His Pro Ala Pro Gly
785 790 795 800

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805 810 815

Val Gly Pro Thr Tyr Met Arg Val Ser
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<210> 3

<211> 327

<212> DNA

<213> Artificial

<220>

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<220>

<221> CDS

<222> (1)..(327)

<400> 3

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gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc 96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

atc ttt ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cct 288
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

ccg tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa 327
 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 4
 <211> 109
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 4

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

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<222> (1)..(327)

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gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc aac agc 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Ser
 20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

atc tat ggt gca tcc agc agg gcc cct ggc atc cca gac agg ttc agt 192
 Ile Tyr Gly Ala Ser Ser Arg Ala Pro Gly Ile Pro Asp Arg Phe Ser
 50 55 60

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

cct gaa gat ttt gca gtg tat tac tgt cag cag tat gat cac tca gca 288
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp His Ser Ala
 85 90 95

ggg tgg acg ttc ggc caa ggg acc aag gtg gag atc aaa 327
 Gly Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

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<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Pro Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp His Ser Ala
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Gly Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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<222> (1)..(327)

<400> 7
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1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag act gtt aac agc gac 96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr Val Asn Ser Asp
20 25 30

tac tta gcc tgg tac cag cag aaa ccg ggc cag gct ccc agg ctc ctc 144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

cct gaa gat ttt gca gtc tat tac tgt cag cag tat ggt agg tca cct 288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg Ser Pro
85 90 95

ccg tgg acg ttc ggc caa ggg acc aaa gtg gat atc aaa 327
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
100 105

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<212> PRT
<213> Artificial

<220>

<223> Synthetic Construct

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 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg Ser Pro
 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
 100 105

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<211> 327

<212> DNA

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<222> (1)..(327)

<400> 9

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 1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc gac 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asp
 20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

atc tat ggt gca tct agc agg gcc tct ggc atc cca gac agg ttc agt 192
 Ile Tyr Gly Ala Ser Ser Arg Ala Ser Gly Ile Pro Asp Arg Phe Ser
 50 55 60

ggc agt ggg ttt ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
 Gly Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

cct gaa gat ttt gca ata tat tac tgt cag cag tat ggt agc tca cct 288
 Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

ccg tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa 327
 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 10

<211> 109

<212> PRT

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<223> Synthetic Construct

<400> 10

Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asp
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Ser Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

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<212> DNA

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<222> (1)..(327)

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gaa	aga	gcc	acc	ctc	tcc	tgc	agg	gcc	agt	cag	agt	gtt	aac	agc	aac	96
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Asn	Ser	Asn	
			20					25					30			

tac	tta	gcc	tgg	tac	cag	cag	aaa	cct	ggc	cag	gct	ccc	agg	ctc	ctc	144
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	
		35					40					45				

atc	tat	ggg	aca	tcc	tac	agg	gcc	act	ggc	atc	cca	gac	agg	ttc	agt	192
Ile	Tyr	Gly	Thr	Ser	Tyr	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser	
	50					55					60					

ggc	agt	ggg	tct	ggg	aca	gac	ttc	act	ctc	acc	atc	acc	aga	ctg	gag	240
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Thr	Arg	Leu	Glu	
65					70					75				80		

cct	gaa	gat	ttt	gca	gtg	tat	tac	tgt	cag	cag	tat	ggg	agc	tca	cca	288
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro	
			85					90						95		

ccg	tgg	acg	ttc	ggc	caa	ggg	aca	cga	ctg	gag	att	aaa				327
Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys				
			100					105								

<210> 12

<211> 109

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 12

Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	

Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Asn	Ser	Asn
			20					25					30		

Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
		35					40					45			

Ile Tyr Gly Thr Ser Tyr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
 100 105

<210> 13

<211> 327

<212> DNA

<213> Artificial

<220>

<223> Light chain variable sequence

<220>

<221> CDS

<222> (1)..(327)

<400> 13

gat att gtg ctg acg cag act cca gcc acc ctg tct ttg tct cca ggg 48
 Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt ggc agc agc 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
 20 25 30

tac tta gcc tgg tac cag cag aga cct ggc cag gct ccc agg ctc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

atc tat ggt gca tcc agc agg gcc act ggc atc ccg gac agg ttc agt 192
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

ggc agt ggg tct ggg aca gac ttc act ctc acg atc agc aga ctg gag 240
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

cct gaa gat ttt gca gtg tat tat tgt cag cag tat gga agt tca cct 288
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

ccg tgg atg ttc ggc caa ggg acc aag gtg gag atc aaa 327
 Pro Trp Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 14

<211> 109

<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 14

Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Pro Trp Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 15
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 15
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15
tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45


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tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag      192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
  50                      55                      60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt      240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
  65                      70                      75                      80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca      288
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
                      85                      90                      95

aga ggg agg tac tac ttt gac tac tgg ggc cag gga acc ctg gtc acc      336
Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
                      100                      105                      110

gtc tcc tca
Val Ser Ser
  115

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<210> 16
<211> 115
<212> PRT
<213> Artificial

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<220>
<223> Synthetic Construct

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<400> 16

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Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
  1                      5                      10                      15

```

```

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
          20                      25                      30

```

```

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35                      40                      45

```

```

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
  50                      55                      60

```

```

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
  65                      70                      75                      80

```

```

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
          85                      90                      95

```

```

Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
          100                      105                      110

```

Val Ser Ser
115

<210> 17
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 17
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
1 5 10 15
tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80
caa atg aac agc ctg agt gcc gag gac atg gct gtg tat tac tgt gca 288
Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95
aga ggg agg tac tac ttc acc cac tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
gtc tcc tca 345
Val Ser Ser
115

<210> 18
<211> 115
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 18

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 19
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 19
 gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg tac aac aac tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 20
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 20

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 21
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 21
 gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95
 aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 gtc tcc tca 345
 Val Ser Ser
 115

<210> 22
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 22

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 23
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 23
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15
tcc ctg aga ctg tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tac ttc acg agg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 24
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 24

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 25
 <211> 345
 <212> DNA
 <213> Artificial

<220>

<223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)..(345)

<400> 25

gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg	48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly	
1 5 10 15	

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat	96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta	144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag	192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys	
50 55 60	

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca	288
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala	
85 90 95	

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc	336
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	

gtc tcc tca	345
Val Ser Ser	
115	

<210> 26

<211> 115

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 26

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 27
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 27
 gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 28
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 28

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 29
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)..(345)

<400> 29

gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 30

<211> 115

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 30

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 31
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 31
 gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95
 aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca
Val Ser Ser
115

345

<210> 32
<211> 115
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 32

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 33
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 33
gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15
tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80
caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95
aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
gtc tcc tca 345
Val Ser Ser
115

<210> 34
<211> 115
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 34

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 35

<211> 345

<212> DNA

<213> Artificial

<220>

<223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)..(345)

<400> 35

gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

gtc tcc tca 345
Val Ser Ser
115

<210> 36
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 36

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 37
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 37

gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

48

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 38
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 38

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

$\langle 210 \rangle$	40
$\langle 211 \rangle$	115

<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 40

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 41
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 41
gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr, Tyr Cys Ala
 85 90 95

aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 42
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 42

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 43
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 43
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 aga ggg agg tac tac ttt gac tac tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 gtc tcc tca 345
 Val Ser Ser
 115

<210> 44
 <211> 115
 <212> PRT
 <213> Artificial

<220>

<223> Synthetic Construct

<400> 44

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 45

<211> 345

<212> DNA

<213> Artificial

<220>

<223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)..(345)

<400> 45

gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

aga ggg agg tac tac ttc acc cac tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

gtc tcc tca 345
Val Ser Ser
115

<210> 46
<211> 115
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 46

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 47
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 47
gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
aga ggg agg tac tgg tac aac aac tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
gtc tcc tca 345
Val Ser Ser
115

<210> 48
<211> 115
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 48

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 49

<211> 345

<212> DNA

<213> Artificial

<220>

<223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)..(345)

<400> 49

gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 aga ggg agg tac tac ttc acg agg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 gtc tcc tca 345
 Val Ser Ser
 115

<210> 50
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 50

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 51
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 51
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 gtc tcc tca 345
 Val Ser Ser
 115

<210> 52
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 52
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 53
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 53
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg tac ccg tgg tgg gcc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 54
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 54

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 55
 <211> 345

<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 55
gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
gtc tcc tca 345
Val Ser Ser
115

<210> 56
<211> 115
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 56
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 57
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 57
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 95

aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 58
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 58

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 59
 <211> 345
 <212> DNA
 <213> Artificial

<220>

<223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)..(345)

<400> 59

gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg	48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta	144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag	192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50 55 60	

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca	288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc	336
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	

gtc tcc tca	345
Val Ser Ser	
115	

<210> 60

<211> 115

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 60

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 61
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 61
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 62
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 62

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 63
 <211> 109
 <212> PRT
 <213> Artificial

<220>
 <223> 27A1 light chain variable region

<400> 63

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 64
 <211> 116
 <212> PRT
 <213> Artificial

<220>
 <223> 27A1 heavy chain variable region

<400> 64

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
 35 40 45

Ala Ile Ile Trp Phe Glu Gly Asn Asn Gln Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Lys Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 65
 <211> 107
 <212> PRT
 <213> Artificial

<220>
 <223> 5A1 light chain variable region

<400> 65

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr His Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 66
 <211> 123
 <212> PRT
 <213> Artificial

<220>
 <223> 5A1 heavy chain variable region

<400> 66

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Thr Cys Ala Gly Ser Gly Phe Thr Phe Ser Asn Phe
20 25 30

Val Met His Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Arg Pro Met Val Arg Gly Val Ile Ile Asp Tyr Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 67
<211> 107
<212> PRT
<213> Artificial

<220>
<223> 63 light chain variable region

<400> 67

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Trp
20 25 30

Leu Ala Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105

<210> 68
 <211> 117
 <212> PRT
 <213> Artificial

<220>
 <223> 63 heavy chain variable region

<400> 68

Glu Val Gln Val Leu Glu Ser Gly Gly Asn Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Phe Tyr Cys
 85 90 95

Ala Lys Asp Asn Arg Gly Phe Phe His Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 69
 <211> 107
 <212> PRT
 <213> Artificial

<220>
 <223> 1B7 light chain variable region

<400> 69

Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Arg
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ile Ala Ser Ile Leu Gln Arg Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe
 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105

<210> 70
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> Primers

<220>
 <221> misc_feature
 <222> (21)..(21)
 <223> N is A or G

<220>
 <221> misc_feature
 <222> (24)..(24)
 <223> N is G or T

<400> 70
 gtcgacgccg ccaccatgga nttngggctg agctgg

36

<210> 71
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> Primers

<400> 71
 cttgaccagg cagcccaggg c

21

<210> 72
<211> 36
<212> DNA
<213> Artificial

<220>
<223> Primers

<400> 72
atcaaacgta cgggtggctgc accatctgtc ttcacg 36

<210> 73
<211> 49
<212> DNA
<213> Artificial

<220>
<223> Primers

<400> 73
gtttaaacgc ggccgcggat cctaacactc tcccctgttg aagctcttt 49

<210> 74
<211> 99
<212> DNA
<213> Artificial

<220>
<223> Primers

<400> 74
gtcgacgccg ccacccatgga aaccccagcg cagcttctct tcctoctgct actctggctc 60
ccagataccg ctagcgaaat tgtgttgacg cagtctcca 99

<210> 75
<211> 99
<212> DNA
<213> Artificial

<220>
<223> Primers

<400> 75
tggagactgc gtcaacacaa tttcgctagc ggtatctggg agccagagta gcaggaggaa 60
gagaagctgc gctgggggttt ccatggtggc ggcgtcgac 99

<210> 76
<211> 57
<212> DNA
<213> Artificial

<220>
<223> Primers

<400> 76
 atgggggtcaa cgcgcacacct tggcctcctc ctggctgttc tccaaggagt cgctagc 57

<210> 77
 <211> 327
 <212> PRT
 <213> Homo sapiens

<400> 77
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15
 Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
 65 70 75 80
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
 100 105 110
 Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 115 120 125
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 130 135 140
 Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 145 150 155 160
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
325